## Serial No.: 10/718,342

## Claim Amendments

1. (currently amended) A method for selecting a combination of nucleic acid sample pairs for evaluating the ability of an oligonucleotide probe to measure differential expression of genes, said method comprising:

- (a) conducting differential expression experiments using (i) nucleic acid sample pairs wherein the pairs comprise different nucleic acid samples and (ii) nucleic acid probes immobilized on a substrate, said probes representing a set of genes where the number of genes in the set is a portion of an expected number of genes in a sample, and
- (b) selecting a <u>combination of</u> nucleic acid sample <u>pairs pair combination</u> in relation to the members of said combination having a maximized number of genes from the set of genes that exhibit differential expression and a minimized number of <u>said</u> genes <u>from the set of genes</u> that do not exhibit differential expression.
- 2. (currently amended) A method according to Claim 1 wherein a determination is made for each gene in the set of genes in step (a) whether the gene is differentially expressed and whether probes representing a set of genes for each gene cluster together.
- 3. (original) A method according to Claim 2 wherein said determination is made based on one or more parameters from said differential expression experiments.
- 4. (original) A method according to Claim 3 wherein said parameters are selected from the group consisting of LogRatio, LogRatio error and signal intensities.
- 5. (currently amended) A method according to Claim 3 wherein said parameters are (i) the probability of a combined LogRatio value being significantly different from zero for each of said probes representing a gene and (ii) the number of probes for a gene that have a probability of the combined LogRatio value being significantly different from zero above a threshold value.
- 6. (original) A method according to Claim 1 wherein said nucleic acid sample pairs are tissue pairs.

Attorney Docket No. 10030679-1

Serial No.: 10/718,342

7. (original) A method according to Claim 1 wherein in step (a) said differential expression experiments are conducted by contacting a nucleic acid sample pair with a substrate having said nucleic acid probes immobilized thereon.

- 8. (original) A method according to Claim 1 wherein in step (a) said differential expression experiments are conducted by contacting each member of a nucleic acid sample pair with a separate substrate having said nucleic acid probes immobilized thereon.
- 9. (currently amended) A method for selecting a combination of nucleic acid sample pairs for evaluating the ability of an oligonucleotide probe to measure differential expression of genes, said method comprising:
- (a) contacting each nucleic acid sample pair from a plurality of nucleic acid sample pairs with a plurality of probes for each of a predetermined number of genes to determine whether said genes exhibit differential expression wherein the nucleic acid sample pairs comprise different nucleic acid samples,
- determining for each gene and each of said nucleic acid sample pairs whether (b) said gene exhibits or does not exhibit differential expression based on one or more parameters,
- for a gene that exhibits differential expression in step (b) for a nucleic acid (c) sample pair, assigning a "yes" value, and for each gene that does not exhibit differential expression in step (b) for a nucleic acid sample pair, assigning a "no" value thereby collecting data,
- (d) tabulating the data from step (c) for each combination of said nucleic acid sample pairs to be evaluated, and
- selecting a combination of nucleic acid sample pairs having a score based on a (e) maximized number of "yes's" and a minimized number of "no's."
- 10. (original) A method according to Claim 9 wherein said parameters are selected from the group consisting of LogRatio, LogRatio error and signal intensities.
- 11. (original) A method according to Claim 9 wherein said nucleic acid sample pairs are tissue pairs.

Claims 12-19 (canceled).

Serial No.: 10/718,342 Attorney Docket No. 10030679-1

20. (original) A method of identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for a target nucleic acid, said method comprising evaluating the sequence using nucleic acid sample pairs selected by a method of claim 1.

- 21. (currently amended) A method of identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for a target nucleic acid, said method comprising:
- (a) identifying a plurality of candidate <u>nucleic acid</u> probe sequences for said target nucleic acid based on at least one selection criterion;
- (b) empirically evaluating each of said candidate <u>nucleic acid</u> probe sequences under a plurality of different experimental sets to obtain a collection of empirical data values for each of said candidate nucleic acid probe sequences for each of said plurality of different experimental sets wherein said empirical evaluation employs a nucleic acid sample pair selected by a method according to Claim 1;
- (c) clustering said candidate <u>nucleic acid</u> probe sequences into one or more groups of candidate <u>nucleic acid</u> probe sequences based on each candidate <u>nucleic acid</u> probe sequence's collection of empirical data values, wherein each of said one or more groups exhibits substantially the same performance across said plurality of experimental sets;
  - (d) selecting one of said one or more groups based on at least one criterion; and
- (e) choosing a candidate <u>nucleic acid</u> probe sequence from said selected group to as said sequence of said nucleic acid that is suitable for use as a substrate immobilized probe for said target nucleic acid.
- 22. (original) A method of producing an array of nucleic acids on the surface of a substrate, said method comprising:
  - (a) identifying nucleic acid probes by a method according to Claim 21 and
- (b) synthesizing or depositing said nucleic acid probes identified in step (a) in an array on the surface of a substrate.
- 23. (original) A method of detecting the presence of a nucleic acid analyte in a sample, said method comprising:
- (a) contacting a nucleic acid array produced according to Claim 22 with said sample and

Serial No.: 10/718,342 Attorney Docket No. 10030679-1

(b) detecting the presence of binding complexes on the surface of said array to detect the presence of said analyte in said sample.

- 24. (original) A method comprising forwarding data representing a result obtained from a method of Claim 23.
- 25. (original) A method according to claim 23 wherein the data is transmitted to a remote location.
- 26. (original) A method comprising receiving data representing a result obtained from a method of Claim 23.

Claims 27-28 (canceled).